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SEQUENCE LISTING FREE TEXT

SEQ ID NO: 1

Designed oligonucleotide primer to amplify bchH

5 gene

SEQ ID NO: 2

Designed oligonucleotide primer to amplify bchH

gene

SEQ ID NO: 3

10 Designed oligonucleotide primer to amplify
soybean PPO gene

SEQ ID NO: 4

Designed oligonucleotide primer to amplify
soybean PPO gene

15 SEQ ID NO: 7

Designed oligonucleotide primer to amplify bchH

gene

SEQ ID NO: 8

Designed oligonucleotide primer to amplify bchH

20 gene

SEQ ID NO: 9

Designed oligonucleotide primer to amplify DNA
fragment having partial sequence of tobacco chlH gene

SEQ ID NO: 10

25 Designed oligonucleotide primer to amplify DNA

002207-0726560

fragment having partial sequence of tobacco chlH gene

SEQ ID NO: 11

Designed oligonucleotide primer to amplify DNA

fragment having partial sequence of soybean PPO gene

5 SEQ ID NO: 12

Designed oligonucleotide primer to amplify DNA

fragment having partial sequence of soybean PPO gene

SEQ ID NO: 13

Designed oligonucleotide primer to amplify DNA

10 fragment having partial sequence of soybean PPO gene

SEQ ID NO: 14

Designed oligonucleotide primer to amplify DNA

fragment having partial sequence of soybean PPO gene

SEQ ID NO: 15

15 Designed oligonucleotide primer to amplify

Chlamydomonas PPO gene

SEQ ID NO: 16

Designed oligonucleotide primer to amplify

Chlamydomonas PPO gene

20 SEQ ID NO: 19

Designed oligonucleotide primer to amplify DNA

fragment having partial sequence of *Chlamydomonas* PPO gene

SEQ ID NO: 20

Designed oligonucleotide primer to amplify DNA

25 fragment having partial sequence of *Chlamydomonas* PPO gene

0042001-01220500

SEQ ID NO: 21

Designed oligonucleotide primer to amplify DNA fragment having partial sequence of cucumber ferrochelatase gene

5 SEQ ID NO: 22

Designed oligonucleotide primer to amplify DNA fragment having partial sequence of cucumber ferrochelatase gene

SEQ ID NO: 23

10 Designed oligonucleotide primer to amplify *Escherichia coli* hemF gene

SEQ ID NO: 24

Designed oligonucleotide primer to amplify *Escherichia coli* hemF gene

15 SEQ ID NO: 25

Designed oligonucleotide primer to amplify *Escherichia coli* hemF gene

SEQ ID NO: 26

20 Designed oligonucleotide primer to amplify *Escherichia coli* hemF gene

SEQ ID NO: 27

Designed oligonucleotides to synthesize genes encoding random peptides comprising 5 amino acids

SEQ ID NO: 28

25 Designed oligonucleotides to synthesize genes

002207-0726560

encoding random peptides comprising 5 amino acids

SEQ ID NO: 29

Designed oligonucleotide to synthesize the gene
encoding the peptide HASYS

5

SEQ ID NO: 30

Designed oligonucleotide to synthesize the gene
encoding the peptide HASYS

SEQ ID NO: 31

10

Designed oligonucleotide to synthesize the gene
encoding the peptide RASSL

SEQ ID NO: 32

Designed oligonucleotide to synthesize the gene
encoding the peptide RASSL

SEQ ID NO: 33

15

Designed oligonucleotide to synthesize the gene
encoding the peptide MGHASYS

SEQ ID NO: 34

Designed oligonucleotide to synthesize the gene
encoding the peptide MGHASYS

20

SEQ ID NO: 35

Designed oligonucleotide to synthesize the gene
encoding the peptide MGRASSL

SEQ ID NO: 36

Designed oligonucleotide to synthesize the gene
25 encoding the peptide MGRASSL

0060710103700

SEQ ID NO: 37

Designed oligonucleotide to synthesize the gene
encoding the peptide MGYAGY

SEQ ID NO: 38

5 Designed oligonucleotide to synthesize the gene
encoding the peptide MGYAGY

SEQ ID NO: 39

Designed oligonucleotide to synthesize the gene
encoding the peptide MGYAGF

10 SEQ ID NO: 40

Designed oligonucleotide to synthesize the gene
encoding the peptide MGYAGF

SEQ ID NO: 41

15 Designed oligonucleotide to synthesize the gene
encoding the peptide MG(HASYS)4

SEQ ID NO: 42

Designed oligonucleotide to synthesize the gene
encoding the peptide MG(HASYS)4

SEQ ID NO: 43

20 Designed oligonucleotide to synthesize the gene
encoding the peptide MG(HASYS)4

SEQ ID NO: 44

Designed oligonucleotide to synthesize the gene
encoding the peptide MG(HASYS)4

25 SEQ ID NO: 45

0050710-102700

Designed oligonucleotide to synthesize the gene
encoding the peptide MG(HASYS)8

SEQ ID NO: 46

5 Designed oligonucleotide to synthesize the gene
encoding the peptide MG(HASYS)8

SEQ ID NO: 47

Designed oligonucleotide to synthesize the gene
encoding the peptide MG(RASSL)4

SEQ ID NO: 48

10 Designed oligonucleotide to synthesize the gene
encoding the peptide MG(RASSL)4

SEQ ID NO: 49

Designed oligonucleotide to synthesize the gene
encoding the peptide MG(RASSL)4

5 SEQ ID NO: 50

Designed oligonucleotide to synthesize the gene
encoding the peptide MG(RASSL)4

SEQ ID NO: 51

20 Designed oligonucleotide to synthesize the gene
encoding the peptide MG(RASSL)8

SEQ ID NO: 52

Designed oligonucleotide to synthesize the gene
encoding the peptide MG(RASSL)8

SEQ ID NO: 53

25 Protoporphyrin IX binding protein HASYS

SEQ ID NO: 54

Protoporphyrin IX binding protein MGHASYS

SEQ ID NO: 55

Protoporphyrin IX binding protein RASSL

5

SEQ ID NO: 56

Protoporphyrin IX binding protein MGRASSL

SEQ ID NO: 57

H₂TMpyP binding protein YAGY

SEQ ID NO: 58

10

H₂TMpyP binding protein MGYAGY

SEQ ID NO: 59

H₂TMpyP binding protein YAGF

SEQ ID NO: 60

H₂TMpyP binding protein MGYAGF

15

SEQ ID NO: 61

Protoporphyrin IX binding protein MG(HASYS)₄

SEQ ID NO: 62

Protoporphyrin IX binding protein MG(HASYS)₈

SEQ ID NO: 63

20

Protoporphyrin IX binding protein MG(RASSL)₄

SEQ ID NO: 64

Protoporphyrin IX binding protein MG(RASSL)₈

SEQ ID NO: 65

25

Designed oligonucleotide primer to introduce
mutation into arabidopsis PPO gene

00597719-102700

SEQ ID NO: 66

Designed oligonucleotide primer to amplify
herbicide resistant arabidopsis PPO(A220V) gene

SEQ ID NO: 67

5 Designed oligonucleotide primer to amplify
herbicide resistant arabidopsis PPO(A220V) gene

SEQ ID NO: 68

Designed oligonucleotide primer to amplify
arabidopsis chloroplast ferrochelataase gene

10 SEQ ID NO: 69

Designed oligonucleotide primer to amplify
arabidopsis chloroplast ferrochelataase gene

SEQ ID NO: 70

15 Designed oligonucleotide primer to amplify
soybean coproporphyrinogen III oxidase gene

SEQ ID NO: 71

Designed oligonucleotide primer to amplify
soybean coproporphyrinogen III oxidase gene

SEQ ID NO: 72

20 Designed oligonucleotide primer to amplify DNA
fragment having nucleotide sequence encoding the Petunia
hybrida EPSPS chloroplast transit peptide and the
Agrobacterium sp. strain CP4 EPSPS gene

SEQ ID NO: 73

25 Designed oligonucleotide primer to amplify DNA

00507740-103700

fragment having nucleotide sequence encoding the *Petunia hybrida* EPSPS chloroplast transit peptide and the *Agrobacterium* sp. strain CP4 EPSPS gene

SEQ ID NO: 75

- 5 Designed oligonucleotide primer to amplify DNA fragment having partial sequence of soybean PPO gene

SEQ ID NO: 76

 Designed oligonucleotide primer to amplify DNA fragment having partial sequence of soybean PPO gene

002227-012500

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15

20

<160> 76

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<400> 1

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10 <210> 2

<211> 31

<212> DNA

<213> Artificial Sequence

15 <220>

<223> Designed oligonucleotide primer to amplify bchH gene

<400> 2

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<210> 3

<211> 39

<212> DNA

<213> Artificial Sequence

002201-61225500

<220>

<223> Designed oligonucleotide primer to amplify soybean PPO gene

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<210> 4

<211> 39

<212> DNA

10 <213> Artificial Sequence

<220>

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15 <400> 4

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<210> 5

<211> 1632

20 <212> DNA

<213> Glycine max var. Williams82

<220>

<221> CDS

25 <222> (1)... (1632)

002201-61426960

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5 ctt cgc ccc tcc ctc cat tcc cca acc tct ttc ttc acc tct ccc act 96
Leu Arg Pro Ser Leu His Ser Pro Thr Ser Phe Phe Thr Ser Pro Thr

cga aaa ttc cct cgc tct cgc cct aac cct att cta cgc tgc tcc att 144
Arg Lys Phe Pro Arg Ser Arg Pro Asn Pro Ile Leu Arg Cys Ser Ile

gcg gag gaa tcc acc gcg tct ccg ccc aaa acc aga gac tcc gcc ccc 192
Ala Glu Glu Ser Thr Ala Ser Pro Pro Lys Thr Arg Asp Ser Ala Pro

gtg gac tgc gtc gtc gtc ggc gga ggc gtc agc ggc ctc tgc atc gcc 240
15 Val Asp Cys Val Val Val Gly Gly Gly Val Ser Gly Leu Cys Ile Ala

cag gcc ctc gcc acc aaa cac gcc aat gcc aac gtc gtc gtc acg gag 288
Gln Ala Leu Ala Thr Lys His Ala Asn Ala Asn Val Val Val Thr Glu

20 gcc cga gac cgc gtc ggc ggc aac atc acc acg atg gag agg gac gga 336
Ala Arg Asp Arg Val Gly Gly Asn Ile Thr Thr Met Glu Arg Asp Gly

Tac ctc tgg gaa gaa ggc ccc aac agc ttc cag cct tct gat cca atg 384
Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met

25 115 120 125

ctc acc atg gtg gtg gac agt ggt tta aag gat gag ctt gtt ttg ggg 432
 Leu Thr Met Val Val Asp Ser Gly Leu Lys Asp Glu Leu Val Leu Gly
 130 135 140
 gat cct gat gca cct cgg ttt gtg ttg tgg aac agg aag ttg agg ccg 480
 5 Asp Pro Asp Ala Pro Arg Phe Val Leu Trp Asn Arg Lys Leu Arg Pro
 145 150 155 160
 gtg ccc ggg aag ctg act gat ttg cct ttc ttt gac ttg atg agc att 528
 Val Pro Gly Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile
 165 170 175
 10 ggt ggc aaa atc agg gct ggc ttt ggt gcg ctt gga att cgg cct cct 576
 Gly Gly Lys Ile Arg Ala Gly Phe Gly Ala Leu Gly Ile Arg Pro Pro
 180 185 190
 cct cca ggt cat gag gaa tcg gtt gaa gag ttt gtt cgt cgg aac ctt 624
 Pro Pro Gly His Glu Glu Ser Val Glu Glu Phe Val Arg Arg Asn Leu
 15 195 200 205
 ggt gat gag gtt ttt gaa cgg ttg ata gag cct ttt tgt tca ggg gtc 672
 Gly Asp Glu Val Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val
 210 215 220
 tat gca ggc gat cct tca aaa tta agt atg aaa gca gca ttc ggg aaa 720
 20 Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys
 225 230 235 240
 gtt tgg aag ctg gaa aaa aat ggt ggt agc att att ggt gga act ttc 768
 Val Trp Lys Leu Glu Lys Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe
 245 250 255

002201-002200

	aaa gca ata caa gag aga aat gga gct tca aaa cca cct cga gat ccg	816
	Lys Ala Ile Gln Glu Arg Asn Gly Ala Ser Lys Pro Pro Arg Asp Pro	
	260 265 270	
	cgt ctg cca aaa cca aaa ggt cag act gtt gga tct ttc cgg aag gga	864
5	Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly	
	275 280 285	
	ctt acc atg ttg cct gat gca att tct gcc aga cta ggc aac aaa gta	912
	Leu Thr Met Leu Pro Asp Ala Ile Ser Ala Arg Leu Gly Asn Lys Val	
	290 295 300	
10	aag tta tct tgg aag ctt tca agt att agt aaa ctg gat agt gga gag	960
	Lys Leu Ser Trp Lys Leu Ser Ser Ile Ser Lys Leu Asp Ser Gly Glu	
	305 310 315 320	
	tac agt ttg aca tat gaa aca cca gaa gga gtg gtt tct ttg cag tgc	1008
	Tyr Ser Leu Thr Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Cys	
15	325 330 335	
	aaa act gtt gtc ctg acc att cct tcc tat gtt gct agt aca ttg ctg	1056
	Lys Thr Val Val Leu Thr Ile Pro Ser Tyr Val Ala Ser Thr Leu Leu	
	340 345 350	
	cgt cct ctg tct gct gct gct gca gat gca ctt tca aag ttt tat tac	1104
20	Arg Pro Leu Ser Ala Ala Ala Ala Asp Ala Leu Ser Lys Phe Tyr Tyr	
	355 360 365	
	cct cca gtt gct gca gtt tcc ata tcc tat cca aaa gaa gct att aga	1152
	Pro Pro Val Ala Ala Val Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg	
	370 375 380	

tca gaa tgc ttg ata gat ggt gag ttg aag ggg ttt ggt caa ttg cat 1200
 Ser Glu Cys Leu Ile Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His
 385 390 395 400
 cca cgt agc caa gga gtg gaa aca tta gga act ata tac agc tca tca 1248
 5 Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser
 405 410 415
 cta ttc ccc aac cga gca cca cct gga agg gtt cta ctc ttg aat tac 1296
 Leu Phe Pro Asn Arg Ala Pro Pro Gly Arg Val Leu Leu Leu Asn Tyr
 420 425 430
 10 att gga gga gca act aat act gga att tta tcg aag acg gac agt gaa 1344
 Ile Gly Gly Ala Thr Asn Thr Gly Ile Leu Ser Lys Thr Asp Ser Glu
 435 440 445
 ctt gtg gaa aca gtt gat cga gat ttg agg aaa atc ctt ata aac cca 1392
 Leu Val Glu Thr Val Asp Arg Asp Leu Arg Lys Ile Leu Ile Asn Pro
 15 450 455 460
 aat gcc cag gat cca ttt gta gtg ggg gtg aga ctg tgg cct caa gct 1440
 Asn Ala Gln Asp Pro Phe Val Val Gly Val Arg Leu Trp Pro Gln Ala
 465 470 475 480
 att cca cag ttc tta gtt ggc cat ctt gat ctt cta gat gtt gct aaa 1488
 20 Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu Asp Val Ala Lys
 485 490 495
 gct tct atc aga aat act ggg ttt gaa ggg ctc ttc ctt ggg ggt aat 1536
 Ala Ser Ile Arg Asn Thr Gly Phe Glu Gly Leu Phe Leu Gly Gly Asn
 500 505 510

002207:6722960

tat gtg tct ggt gtt gcc ttg gga cga tgc gtt gag gga gcc tat gag 1584

Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu

515

520

525

gta gca gct gaa gta aac gat ttt ctc aca aat aga gtg tac aaa tag 1632

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535

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543

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<213> Glycine max var. Williams82

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Leu Arg Pro Ser Leu His Ser Pro Thr Ser Phe Phe Thr Ser Pro Thr

20

25

30

Arg Lys Phe Pro Arg Ser Arg Pro Asn Pro Ile Leu Arg Cys Ser Ile

35

40

45

20 Ala Glu Glu Ser Thr Ala Ser Pro Pro Lys Thr Arg Asp Ser Ala Pro

50

55

60

Val Asp Cys Val Val Val Gly Gly Gly Val Ser Gly Leu Cys Ile Ala

65

70

75

80

Gln Ala Leu Ala Thr Lys His Ala Asn Ala Asn Val Val Val Thr Glu

25

85

90

95

002201-0126960

Ala Arg Asp Arg Val Gly Gly Asn Ile Thr Thr Met Glu Arg Asp Gly
 100 105 110
 Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met
 115 120 125
 5 Leu Thr Met Val Val Asp Ser Gly Leu Lys Asp Glu Leu Val Leu Gly
 130 135 140
 Asp Pro Asp Ala Pro Arg Phe Val Leu Trp Asn Arg Lys Leu Arg Pro
 145 150 155 160
 Val Pro Gly Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile
 10 165 170 175
 Gly Gly Lys Ile Arg Ala Gly Phe Gly Ala Leu Gly Ile Arg Pro Pro
 180 185 190
 Pro Pro Gly His Glu Glu Ser Val Glu Glu Phe Val Arg Arg Asn Leu
 195 200 205
 15 Gly Asp Glu Val Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val
 210 215 220
 Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys
 225 230 235 240
 Val Trp Lys Leu Glu Lys Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe
 20 245 250 255
 Lys Ala Ile Gln Glu Arg Asn Gly Ala Ser Lys Pro Pro Arg Asp Pro
 260 265 270
 Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly
 275 280 285

002207-0726960

Leu Thr Met Leu Pro Asp Ala Ile Ser Ala Arg Leu Gly Asn Lys Val
 290 295 300
 Lys Leu Ser Trp Lys Leu Ser Ser Ile Ser Lys Leu Asp Ser Gly Glu
 305 310 315 320
 5 Tyr Ser Leu Thr Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Cys
 325 330 335
 Lys Thr Val Val Leu Thr Ile Pro Ser Tyr Val Ala Ser Thr Leu Leu
 340 345 350
 Arg Pro Leu Ser Ala Ala Ala Ala Asp Ala Leu Ser Lys Phe Tyr Tyr
 10 355 360 365
 Pro Pro Val Ala Ala Val Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg
 370 375 380
 Ser Glu Cys Leu Ile Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His
 385 390 395 400
 15 Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser
 405 410 415
 Leu Phe Pro Asn Arg Ala Pro Pro Gly Arg Val Leu Leu Leu Asn Tyr
 420 425 430
 Ile Gly Gly Ala Thr Asn Thr Gly Ile Leu Ser Lys Thr Asp Ser Glu
 20 435 440 445
 Leu Val Glu Thr Val Asp Arg Asp Leu Arg Lys Ile Leu Ile Asn Pro
 450 455 460
 Asn Ala Gln Asp Pro Phe Val Val Gly Val Arg Leu Trp Pro Gln Ala
 465 470 475 480

002220T.01426960

Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu Asp Val Ala Lys

485

490

495

Ala Ser Ile Arg Asn Thr Gly Phe Glu Gly Leu Phe Leu Gly Gly Asn

500

505

510

5 Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu

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520

525

Val Ala Ala Glu Val Asn Asp Phe Leu Thr Asn Arg Val Tyr Lys

530

535

540

543

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<211> 39

<212> DNA

<213> Artificial Sequence

15

<220>

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<400> 7

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<210> 8

<211> 31

<212> DNA

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<213> Artificial Sequence

002220101022200

<220>

<223> Designed oligonucleotide primer to amplify bchH gene

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acggaagctt ggtacctcac tcggcggcaa t 31

<210> 9

<211> 35

10 <212> DNA

<213> Artificial Sequence

<220>

15 <223> Designed oligonucleotide primer to amplify DNA fragment having
partial sequence of tobacco chlH gene

<400> 9

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20 <210> 10

<211> 34

<212> DNA

<213> Artificial Sequence

25 <220>

<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of tobacco chlH gene

<400> 10

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<210> 11

<211> 39

<212> DNA

10 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of soybean PPO gene

15

<400> 11

ggcggaggcg tcaccatggt ctgcatcgcc caggcc 36

<210> 12

20 <211> 36

<212> DNA

<213> Artificial Sequence

<220>

25 <223> Designed oligonucleotide primer to amplify DNA fragment having

partial sequence of soybean PPO gene

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5

<210> 13

<211> 33

<212> DNA

<213> Artificial Sequence

10

<220>

<223> Designed oligonucleotide primer to amplify DNA fragment having
partial sequence of soybean PPO gene

15

<400> 13

cacaggaaag gtaccatggt ctgcacgcc cag 33

<210> 14

<211> 33

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<212> DNA

<213> Artificial Sequence

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<223> Designed oligonucleotide primer to amplify DNA fragment having
partial sequence of soybean PPO gene

25

002201-6122000

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<211> 28

<213> Artificial Sequence

<223> Designed oligonucleotide primer to amplify Chlamydomonas PP0 gene

15 aatgatgttg acccagactc ctgggacc 28

<211> 27

20 <213> Artificial Sequence

<223> Designed oligonucleotide primer to amplify Chlamydomonas PPO gene

<400> 16

tactacacat cccagcaagc gccaatg 27

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5 <211> 1838

<212> DNA

<213> Chlamydomonas reinhardtii CC407

<220>

10 <221> CDS

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1 5 10 15

cgg tcg cag atc cgc tcg gct gcg cac gtc tcc gcc aag gtc gcg cct 94

Arg Ser Gln Ile Arg Ser Ala Ala His Val Ser Ala Lys Val Ala Pro

20 25 30

20 cgg ccc acg cca ttc tcg gtc gcg agc ccc gcg acc gct gcg agc ccc 142

Arg Pro Thr Pro Phe Ser Val Ala Ser Pro Ala Thr Ala Ala Ser Pro

35 40 45

gcg acc gcg gcg gcc cgc cgc aca ctc cac cgc act gct gcg gcg gcc 190

Ala Thr Ala Ala Ala Arg Arg Thr Leu His Arg Thr Ala Ala Ala Ala

25 50 55 60

002201 6122550

act ggt gct ccc acg gcg tcc gga gcc ggc gtc gcc aag acg ctc gac 238
 Thr Gly Ala Pro Thr Ala Ser Gly Ala Gly Val Ala Lys Thr Leu Asp
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 5 Asn Val Tyr Asp Val Ile Val Val Gly Gly Gly Leu Ser Gly Leu Val
 80 85 90 95
 acc ggc cag gcc ctg gcg gct cag cac aaa att cag aac ttc ctt gtt 334
 Thr Gly Gln Ala Leu Ala Ala Gln His Lys Ile Gln Asn Phe Leu Val
 100 105 110
 10 acg gag gct cgc gag cgc gtc ggc ggc aac att acg tcc atg tcg ggc 382
 Thr Glu Ala Arg Glu Arg Val Gly Gly Asn Ile Thr Ser Met Ser Gly
 115 120 125
 gat ggc tac gtg tgg gag gag ggc ccg aac agc ttc cag ccc aac gat 430
 Asp Gly Tyr Val Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Asn Asp
 15 130 135 140
 agc atg ctg cag att gcg gtg gac tct ggc tgc gag aag gac ctt gtg 478
 Ser Met Leu Gln Ile Ala Val Asp Ser Gly Cys Glu Lys Asp Leu Val
 145 150 155
 ttc ggt gac ccc acg gct ccc cgc ttc gtg tgg tgg gag ggc aag ctg 526
 20 Phe Gly Asp Pro Thr Ala Pro Arg Phe Val Trp Trp Glu Gly Lys Leu
 160 165 170 175
 cgc ccc gtg ccc tcg ggc ctg gac gcc ttc acc ttc gac ctc atg tcc 574
 Arg Pro Val Pro Ser Gly Leu Asp Ala Phe Thr Phe Asp Leu Met Ser
 180 185 190

002201 6126960

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 gga gcc atg ccc tcc ttc gag gag agt gtg gag cag ttc atc cgc cgc 670
 5 Gly Ala Met Pro Ser Phe Glu Glu Ser Val Glu Gln Phe Ile Arg Arg
 210 215 220
 aac ctg ggc gat gag gtg ttc ttc cgc ctg atc gag ccc ttc tgc tcc 718
 Asn Leu Gly Asp Glu Val Phe Phe Arg Leu Ile Glu Pro Phe Cys Ser
 225 230 235
 ggc gtg tac gcg ggc gac ccc tcc aag ctg tcc atg aag gcg gcc ttc 766
 10 Gly Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe
 240 245 250 255
 aac agg atc tgg att ctg gag aag aac ggc ggc agc ctg gtg gga ggt 814
 Asn Arg Ile Trp Ile Leu Glu Lys Asn Gly Gly Ser Leu Val Gly Gly
 15 260 265 270
 gcc atc aag ctg ttc cag gaa cgc cag tcc aac ccg gcc ccg ccg cgg 862
 Ala Ile Lys Leu Phe Gln Glu Arg Gln Ser Asn Pro Ala Pro Pro Arg
 275 280 285
 gac ccg cgc ctg ccg ccc aag ccc aag ggc cag acg gtg ggc tcg ttc 910
 20 Asp Pro Arg Leu Pro Pro Lys Pro Lys Gly Gln Thr Val Gly Ser Phe
 290 295 300
 cgc aag ggc ctg aag atg ctg ccg gac gcc att gag cgc aac atc ccc 958
 Arg Lys Gly Leu Lys Met Leu Pro Asp Ala Ile Glu Arg Asn Ile Pro
 305 310 315

gac aag atc cgc gtg aac tgg aag ctg gtg tct ctg ggc cgc gag gcg 1006
 Asp Lys Ile Arg Val Asn Trp Lys Leu Val Ser Leu Gly Arg Glu Ala
 320 325 330 335
 gac ggg cgg tac ggg ctg gtg tac gac acg ccc gag ggc cgt gtc aag 1054
 5 Asp Gly Arg Tyr Gly Leu Val Tyr Asp Thr Pro Glu Gly Arg Val Lys
 340 345 350
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 Val Phe Ala Arg Ala Val Ala Leu Thr Ala Pro Ser Tyr Val Val Ala
 355 360 365
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 Asp Leu Val Lys Glu Gln Ala Pro Ala Ala Ala Glu Ala Leu Gly Ser
 370 375 380
 ttc gac tac ccg ccg gtg ggc gcc gtg acg ctg tcg tac ccg ctg agc 1198
 Phe Asp Tyr Pro Pro Val Gly Ala Val Thr Leu Ser Tyr Pro Leu Ser
 15 385 390 395
 gcc gtg cgg gag gag cgc aag gcc tcg gac ggg tcc gtg ccg ggc ttc 1246
 Ala Val Arg Glu Glu Arg Lys Ala Ser Asp Gly Ser Val Pro Gly Phe
 400 405 410 415
 ggt cag ctg cac ccg cgc acg cag ggc atc acc act ctg ggc acc atc 1294
 20 Gly Gln Leu His Pro Arg Thr Gln Gly Ile Thr Thr Leu Gly Thr Ile
 420 425 430
 tac agc tcc agc ctg ttc ccc ggc cgc gcg ccc gag ggc cac atg ctg 1342
 Tyr Ser Ser Ser Leu Phe Pro Gly Arg Ala Pro Glu Gly His Met Leu
 435 440 445

ctg ctc aac tac atc ggc ggc acc acc aac cgc ggc atc gtc aac cag 1390
 Leu Leu Asn Tyr Ile Gly Gly Thr Thr Asn Arg Gly Ile Val Asn Gln
 450 455 460
 acc acc gag cag ctg gtg gag cag gtg gac aag gac ctg cgc aac atg 1438
 5 Thr Thr Glu Gln Leu Val Glu Gln Val Asp Lys Asp Leu Arg Asn Met
 465 470 475
 gtc atc aag ccc gac gcg ccc aag ccc cgt gtg gtg ggc gtg cgc gtg 1486
 Val Ile Lys Pro Asp Ala Pro Lys Pro Arg Val Val Gly Val Arg Val
 480 485 490 495
 10 tgg ccg cgc gcc atc ccg cag ttc aac ctg ggc cac ctg gag cag ctg 1534
 Trp Pro Arg Ala Ile Pro Gln Phe Asn Leu Gly His Leu Glu Gln Leu
 500 505 510
 gac aag gcg cgc aag gcg ctg gac gcg gcg ggg ctg cag ggc gtg cac 1582
 Asp Lys Ala Arg Lys Ala Leu Asp Ala Ala Gly Leu Gln Gly Val His
 15 515 520 525
 ctg ggg ggc aac tac gtc agc ggt gtg gcc ctg ggc aag gtg gtg gag 1630
 Leu Gly Gly Asn Tyr Val Ser Gly Val Ala Leu Gly Lys Val Val Glu
 530 535 540
 cac ggc tac gag tcc gca gcc aac ctg gcc aag agc gtg tcc aag gcc 1678
 20 His Gly Tyr Glu Ser Ala Ala Asn Leu Ala Lys Ser Val Ser Lys Ala
 545 550 555
 gca gtc aag gcc taa ggggtgcag cagtagcagc agcagcatcg ggctgtagct 1733
 Ala Val Lys Ala
 560 563
 25 ggtaaatgcc gcagtggcac cggcagcagc aattggcaag cacttggggc aagcggagtg 1793

gaggcgaggg gggggctacc attggcgctt gctgggatgt gtagt

1838

<210> 18

<211> 563

5 <212> PRT

<213> Chlamydomonas reinhardtii CC407

<400> 18

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 20 25 30
 Arg Pro Thr Pro Phe Ser Val Ala Ser Pro Ala Thr Ala Ala Ser Pro
 15 35 40 45
 Ala Thr Ala Ala Ala Arg Arg Thr Leu His Arg Thr Ala Ala Ala Ala
 50 55 60
 Thr Gly Ala Pro Thr Ala Ser Gly Ala Gly Val Ala Lys Thr Leu Asp
 65 70 75
 20 Asn Val Tyr Asp Val Ile Val Val Gly Gly Gly Leu Ser Gly Leu Val
 80 85 90 95
 Thr Gly Gln Ala Leu Ala Ala Gln His Lys Ile Gln Asn Phe Leu Val
 100 105 110
 Thr Glu Ala Arg Glu Arg Val Gly Gly Asn Ile Thr Ser Met Ser Gly
 25 115 120 125

002201-012200

130 135 140
Ser Met Leu Gln Ile Ala Val Asp Ser Gly Cys Glu Lys Asp Leu Val
145 150 155

10

15

20

Ala Ile Lys Leu Phe Gln Glu Arg Gln Ser Asn Pro Ala Pro Pro Arg
275 280 285

Arg Lys Gly Leu Lys Met Leu Pro Asp Ala Ile Glu Arg Asn Ile Pro
305 310 315

Asp Lys Ile Arg Val Asn Trp Lys Leu Val Ser Leu Gly Arg Glu Ala

320 325 330 335

Asp Gly Arg Tyr Gly Leu Val Tyr Asp Thr Pro Glu Gly Arg Val Lys

340 345 350

5 Val Phe Ala Arg Ala Val Ala Leu Thr Ala Pro Ser Tyr Val Val Ala

355 360 365

Asp Leu Val Lys Glu Gln Ala Pro Ala Ala Ala Glu Ala Leu Gly Ser

370 375 380

Phe Asp Tyr Pro Pro Val Gly Ala Val Thr Leu Ser Tyr Pro Leu Ser

385 390 395

Ala Val Arg Glu Glu Arg Lys Ala Ser Asp Gly Ser Val Pro Gly Phe

400 405 410 415

Gly Gln Leu His Pro Arg Thr Gln Gly Ile Thr Thr Leu Gly Thr Ile

420 425 430

15 Tyr Ser Ser Ser Leu Phe Pro Gly Arg Ala Pro Glu Gly His Met Leu

435 440 445

Leu Leu Asn Tyr Ile Gly Gly Thr Thr Asn Arg Gly Ile Val Asn Gln

450 455 460

Thr Thr Glu Gln Leu Val Glu Gln Val Asp Lys Asp Leu Arg Asn Met

20 465 470 475

Val Ile Lys Pro Asp Ala Pro Lys Pro Arg Val Val Gly Val Arg Val

480 485 490 495

Trp Pro Arg Ala Ile Pro Gln Phe Asn Leu Gly His Leu Glu Gln Leu

500 505 510

002201-6122300

Asp Lys Ala Arg Lys Ala Leu Asp Ala Ala Gly Leu Gln Gly Val His

515

520

525

Leu Gly Gly Asn Tyr Val Ser Gly Val Ala Leu Gly Lys Val Val Glu

530

535

540

5 His Gly Tyr Glu Ser Ala Ala Asn Leu Ala Lys Ser Val Ser Lys Ala

545

550

555

Ala Val Lys Ala

560

563

10 <210> 19

<211> 32

<212> DNA

<213> Artificial Sequence

15 <220>

<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of Chlamydomonas PPO gene

<400> 19

20 ggtcggtgga ggggatccga tgctggtgac cg 32

<210> 20

<211> 32

<212> DNA

25 <213> Artificial Sequence

002201-012500

<220>

<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of Chlamydomonas PPO gene

5

<400> 20

gctactgctg cgagctctta ggccttgact gc 32

<210> 21

10

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

15

<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of cucumber ferrochelatase gene

<400> 21

gctttagaat cggatcctat ggcagtggat gac 33

20

<210> 22

<211> 36

<212> DNA

<213> Artificial Sequence

25

<220>

<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of cucumber ferrochelatase gene

5 <400> 22

ggtgaacttc tatttgagct ctcaggtaaa tataag 36

<210> 23

<211> 25

10 <212> DNA

<213> Artificial Sequence

<220>

15 <223> Designed oligonucleotide primer to amplify Esherichia coli hemF gene

<400> 23

gctgaaggcg tgatcagta tttcc 25

20 <210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

25 <220>

20250726

<223> Designed oligonucleotide primer to amplify Esherichia coli hemF gene

<400> 24

5 catcagcctg cagtgcgaaa agtg 24

<210> 25

<211> 26

<212> DNA

10 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify Esherichia coli hemF gene

15

<400> 25

cgaaaaaggg atccgttatg aaaccc 26

<210> 26

20 <211> 23

<212> DNA

<213> Artificial Sequence

<220>

25 <223> Designed oligonucleotide primer to amplify Esherichia coli hemF

gene

<400> 26

gctgttttcc gagctcccgt cac 23

5

<210> 27

<211> 22

<212> DNA

<213> Artificial Sequence

10

<220>

<223> Designed oligonucleotides to synthesize genes encoding random peptides comprising 5 amino acids

15

<400> 27

tggccnnknn knnknnknnk gc 22

<210> 28

<211> 29

20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotides to synthesize genes encoding random peptides comprising 5 amino acids

25

002207-042690

ggccgcmnnm nnnnnnnnnm nggccagct 29

<211> 22

<213> Artificial Sequence

<223> Designed oligonucleotide to synthesize the gene encoding the peptide HASYS

15 tggcccatgc tagttagtcg gc 22

<211> 29

20 <213> Artificial Sequence

<223> Designed oligonucleotide to synthesize the gene encoding the peptide HASYS

<400> 30

tggcgccgac taactagcat gggccagct 29

<210> 31

5 <211> 22

<212> DNA

<213> Artificial Sequence

<220>

10 <223> Designed oligonucleotide to synthesize the gene encoding the
peptide RASSL

<400> 31

tggcccgggc gtcgtcgttg gc 22

15

<210> 32

<211> 29

<212> DNA

<213> Artificial Sequence

20

<220>

<223> Designed oligonucleotide to synthesize the gene encoding the
peptide RASSL

25

<400> 32

002201-012500

ggccgccaac gacgacgccc gggccagct 29

<210> 33

<211> 26

5 <212> DNA

<213> Artificial Sequence

<220>

10 <223> Designed oligonucleotide to synthesize the gene encoding the peptide MGHASYS

<400> 33

catgggtcac gcttcttact cctaag 26

15 <210> 34

<211> 26

<212> DNA

<213> Artificial Sequence

20 <220>

<223> Designed oligonucleotide to synthesize the gene encoding the peptide MGHASYS

<400> 34

25 aattcttagg agtaagaagc gtagacc 26

002201-612690

<210> 35

<211> 26

<212> DNA

5 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide to synthesize the gene encoding the peptide MGRASSL

10

<400> 35

catgggtcgt gcttcttccc tgtaag 26

<210> 36

15

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Designed oligonucleotide to synthesize the gene encoding the peptide MGRASSL

<400> 36

aattcttaca gggaagaagc acgacc 26

25

<210> 37

<211> 23

<212> DNA

<213> Artificial Sequence

5

<220>

<223> Designed oligonucleotide to synthesize the gene encoding the peptide MGYAGY

10

<400> 37

catgggttac gctggctact aag 23

<210> 38

<211> 23

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<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to synthesize the gene encoding the peptide MGYAGY

20

<400> 38

aattcttagt agccagcgta acc 23

25

<210> 39

002207-012550

<212> DNA

5 $\langle 220 \rangle$

10

catgggttac gctggcttct aag 23

<211> 23

15

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20

aattcttaga agccagcgta acc 23

25

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

5 <223> Designed oligonucleotide to synthesize the gene encoding the peptide MG(HASYS)4

<400> 41

catgggtcac gcttcttact cccatgcac ttac 34

10

<210> 42

<211> 34

<212> DNA

<213> Artificial Sequence

15

<220>

<223> Designed oligonucleotide to synthesize the gene encoding the peptide MG(HASYS)4

20

<400> 42

gtgggagtaa gatgcatggg agtaagaagc gtgacc 36

<210> 43

<211> 37

25

<212> DNA

002201-0122500

<213> Artificial Sequence

<220>

5 <223> Designed oligonucleotide to synthesize the gene encoding the
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<400> 43

tcccacgctt cttactccca tgcattctac tcctaag 37

10 <210> 44

<211> 35

<212> DNA

<213> Artificial Sequence

15 <220>

<223> Designed oligonucleotide to synthesize the gene encoding the
peptide MG(HASYS)4

<400> 44

20 aattcttagg agtaagatgc atgggagtaa gaagc 35

<210> 45

<211> 30

<212> DNA

25 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide to synthesize the gene encoding the peptide MG(HASYS)8

5

<400> 45

tcccacgctt cttactccca tgcattttac 30

<210> 46

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<211> 30

<212> DNA

<213> Artificial Sequence

<220>

15

<223> Designed oligonucleotide to synthesize the gene encoding the peptide MG(HASYS)8

<400> 46

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20

<210> 47

<211> 34

<212> DNA

<213> Artificial Sequence

25

<220>

<223> Designed oligonucleotide to synthesize the gene encoding the peptide MG(RASSL)4

5 <400> 47

catgggtcgt gcttcttccc tgcgcgcac ttcc 34

<210> 48

<211> 36

10 <212> DNA

<213> Artificial Sequence

<220>

15 <223> Designed oligonucleotide to synthesize the gene encoding the peptide MG(RASSL)4

<400> 48

acgcagggaa gatgcgcgca gggaagaagc acgacc 36

20 <210> 49

<211> 37

<212> DNA

<213> Artificial Sequence

25 <220>

000001-0120500

<223> Designed oligonucleotide to synthesize the gene encoding the peptide MG(RASSL)4

<400> 49

5 ctgcgtgctt cttccctgcg cgcattcttc ctgtaag 37

<210> 50

<211> 35

<212> DNA

10 <213> Artificial Sequence

<220>

<223> Designed oligonucleotide to synthesize the gene encoding the peptide MG(RASSL)4

15

<400> 50

aattcttaca gggaagatgc gcgcagggaa gaagc 35

<210> 51

20 <211> 30

<212> DNA

<213> Artificial Sequence

<220>

25 <223> Designed oligonucleotide to synthesize the gene encoding the

002201-612590

peptide MG(RASSL)8

<400> 51

ctgcgtgctt cttccctgcg cgcattcttc 30

5

<210> 52

<211> 30

<212> DNA

<213> Artificial Sequence

10

<220>

<223> Designed oligonucleotide to synthesize the gene encoding the peptide MG(RASSL)8

15

<400> 52

acgcagggaa gatgcgcgca gggaagaagc 30

<210> 53

<211> 5

20

<212> PRT

<213> Artificial Sequence

<220>

<223> Protoporphyrin IX binding protein HASYS

25

00207-022550

<400> 53

His Ala Ser Tyr Ser

1 5

5 <210> 54

<211> 7

<212> PRT

<213> Artificial Sequence

10 <220>

<223> Protoporphyrin IX binding protein MGHASYS

<400> 54

Met Gly His Ala Ser Tyr Ser

15 1 5

<210> 55

<211> 5

<212> PRT

20 <213> Artificial Sequence

<220>

<223> Protoporphyrin IX binding protein RASSL

25 <400> 55

0022016122550

1 5

5 $\langle 211 \rangle$ 7

⟨213⟩ Artificial Sequence

10 <223> Protoporphyrin IX binding protein MGRASSL

Met Gly Arg Ala Ser Ser Leu

1 5

<211> 4

<213> Artificial Sequence

<223> H₂TMpyP binding protein YAGY.

25 Tyr Ala Gly Tyr 4

25

<210> 60

<211> 6

<212> PRT

<213> Artificial Sequence

5

<220>

<223> H₂TMpyP binding protein MGYAGF

<400> 60

10 Met Gly Tyr Ala Gly Phe

1

5

<210> 61

<211> 22

15 <212> PRT

<213> Artificial Sequence

<220>

<223> Protoporphyrin IX binding protein MG(HASYS)₄

20

<400> 61

Met Gly His Ala Ser Tyr Ser His Ala Ser Tyr Ser His Ala Ser Tyr

1

5

10

15

Ser His Ala Ser Tyr Ser

25

20

00607719-102700

<210> 62

<211> 42

<212> PRT

5 <213> Artificial Sequence

<220>

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10 <400> 62

Met Gly His Ala Ser Tyr Ser His Ala Ser Tyr Ser His Ala Ser Tyr

1

5

10

15

Ser His Ala Ser Tyr Ser His Ala Ser Tyr Ser His Ala Ser Tyr Ser

20

25

30

15 His Ala Ser Tyr Ser His Ala Ser Tyr Ser

35

40

<210> 63

<211> 22

20 <212> PRT

<213> Artificial Sequence

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<223> Protoporphyrin IX binding protein MG (RASSL)₄

25

0022016126560

<400> 63

Met Gly Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu Arg Ala Ser Ser

1 5 10 15

Leu Arg Ala Ser Ser Leu

5 20

<210> 64

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Protoporphyrin IX binding protein MG(RASSL)₈.

<400> 64

Met Gly Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu Arg Ala Ser Ser

1 5 10 15

Leu Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu

20 25 30

Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu

35 40

<210> 65

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to introduce mutation into
5 arabidopsis PPO gene

<400> 65

tggttcagggtg tttatgttgg tgatccttca aaactg 36

10 <210> 66

<211> 32

<212> DNA

<213> Artificial Sequence

15 <220>

<223> Designed oligonucleotide primer to amplify herbicide resistant
arabidopsis PPO(A220V) gene

<400> 66

20 ccatgcggaa gcttatggag ttatctcttc tc 32

<210> 67

<211> 34

<212> DNA

25 <213> Artificial Sequence

<220>

<213> Designed oligonucleotide primer to amplify herbicide resistant
arabidopsis PPO(A220V) gene

5

<400> 67

gggagattta atgtcgacca ttacttgta agcg 34

<210> 68

10

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

15

<223> Designed oligonucleotide primer to amplify Arabidopsis
chloroplast ferrochelatase gene

<400> 68

gacgggttct gaaatttgga tccatgcagg c 31

20

<210> 69

<211> 31

<212> DNA

<213> Artificial Sequence

25

002201-0122560

<220>

<223> Designed oligonucleotide primer to amplify Arabidopsis
chloroplast ferrochelatase gene

5 <400> 69

cacaaaacca acgagctcct ataggttccg g 31

<210> 70

<211> 30

10 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify soybean
15 coproporphyrinogen III oxidase gene

<400> 70

gaatcggatc cgaagcatga tgcattgtgc 30

20 <210> 71

<211> 30

<212> DNA

<213> Artificial Sequence

25 <220>

002201-6146560

<223> Designed oligonucleotide primer to amplify soybean
coproporphyrinogen III oxidase gene

<400> 71

5 gggggtcgac tgatgaatta gatccattcc 30

<210> 72

<211> 36

<212> DNA

10 <213> Artificial Sequence

<220>

15 <223> Designed oligonucleotide primer to amplify DNA fragment having
nucleotide sequence encoding the Petunia hybrida EPSPS chloroplast
transit peptide and the Agrobacterium sp. strain CP4 EPSPS gene

<400> 72

ggaagcttca agaatggcac aaattaacaa catggc 36

20 <210> 73

<211> 32

<212> DNA

<213> Artificial Sequence

25 <220>

0022016122560

<223>Designed oligonucleotide primer to amplify DNA fragment having nucleotide sequence encoding the *Petunia hybrida* EPSPS chloroplast transit peptide and the *Agrobacterium* sp. strain CP4 EPSPS gene

5 <400> 73

gagtcgacgg tcatcaggca gccttcgtat cg 32

<210> 74

<211> 1587

10 <212> DNA

<213> *Petunia hybrida* EPSPS chloroplast transit peptide and *Agrobacterium* sp. strain CP4 EPSPS

<220>

15 <221> CDS

<222> (1)... (1581)

<400> 74

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1 5 10 15

aat tcc aat ttc cat aaa ccc caa gtt cct aaa tct tca agt ttt ctt 96

Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu

20 25 30

	gtt ttt gga tct aaa aaa ctg aaa aat tca gca aat tct atg ttg gtt	144
	Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val	
	35 40 45	
	ttg aaa aaa gat tca att ttt atg caa aag ttt tgt tcc ttt agg att	192
5	Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile	
	50 55 60	
	tca gca tca gtg gct aca gcc tgc atg ctt cac ggt gca agc agc cgg	240
	Ser Ala Ser Val Ala Thr Ala Cys Met Leu His Gly Ala Ser Ser Arg	
	65 70 75	
10	ccc gca acc gcc cgc aaa tcc tct ggc ctt tcc gga acc gtc cgc att	288
	Pro Ala Thr Ala Arg Lys Ser Ser Gly Leu Ser Gly Thr Val Arg Ile	
	80 85 90 95	
	ccc ggc gac aag tgc atc tcc cac cgg tcc ttc atg ttc ggc ggt ctc	336
	Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu	
15	100 105 110	
	gcg agc ggt gaa acg cgc atc acc ggc ctt ctg gaa ggc gag gac gtc	384
	Ala Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp Val	
	115 120 125	
	atc aat acg ggc aag gcc atg cag gcc atg ggc gcc agg atc cgt aag	432
20	Ile Asn Thr Gly Lys Ala Met Gln Ala Met Gly Ala Arg Ile Arg Lys	
	130 135 140	
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	gaa ggc gac acc tgg atc atc gat ggc gtc ggc aat ggc ggc ctc ctg	480
	Glu Gly Asp Thr Trp Ile Ile Asp Gly Val Gly Asn Gly Gly Leu Leu	
	145 150 155	

0060710-10200

	gcg cct gag gcg ccg ctc gat ttc ggc aat gcc gcc acg ggc tgc cgc	528
	Ala Pro Glu Ala Pro Leu Asp Phe Gly Asn Ala Ala Thr Gly Cys Arg	
	160 165 170 175	
	ctg acc atg ggc ctc gtc ggg gtc tac gat ttc gac agc acc ttc atc	576
5	Leu Thr Met Gly Leu Val Gly Val Tyr Asp Phe Asp Ser Thr Phe Ile	
	180 185 190	
	ggc gac gcc tcg ctc aca aag cgc ccg atg ggc cgc gtg ttg aac ccg	624
	Gly sp Ala Ser Leu Thr Lys Arg Pro Met Gly Arg Val Leu Asn Pro	
	195 200 205	
10	ctg cgc gaa atg ggc gtg cag gtg aaa tcg gaa gac ggt gac cgt ctt	672
	Leu Arg Glu Met Gly Val Gln Val Lys Ser Glu Asp Gly Asp Arg Leu	
	210 215 220	
	ccc gtt acc ttg cgc ggg ccg aag acg ccg acg ccg atc acc tac cgc	720
	Pro Val Thr Leu Arg Gly Pro Lys Thr Pro Thr Pro Ile Thr Tyr Arg	
15	225 230 235	
	gtg ccg atg gcc tcc gca cag gtg aag tcc gcc gtg ctg ctc gcc ggc	768
	Val Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Leu Ala Gly	
	240 245 250 255	
	ctc aac acg ccc ggc atc acg acg gtc atc gag ccg atc atg acg cgc	816
20	Leu Asn Thr Pro Gly Ile Thr Thr Val Ile Glu Pro Ile Met Thr Arg	
	260 265 270	
	gat cat acg gaa aag atg ctg cag ggc ttt ggc gcc aac ctt acc gtc	864
	Asp His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asn Leu Thr Val	
	275 280 285	

		gag acg gat gcg gac ggc gtg cgc acc atc cgc ctg gaa ggc cgc ggc	912
		Glu Thr Asp Ala Asp Gly Val Arg Thr Ile Arg Leu Glu Gly Arg Gly	
		290 295 300	
		aag ctc acc ggc caa gtc atc gac gtg ccg ggc gac ccg tcc tcg acg	960
5		Lys Leu Thr Gly Gln Val Ile Asp Val Pro Gly Asp Pro Ser Ser Thr	
		305 310 315	
		gcc ttc ccg ctg gtt gcg gcc ctg ctt gtt ccg ggc tcc gac gtc acc	1008
		Ala Phe Pro Leu Val Ala Ala Leu Leu Val Pro Gly Ser Asp Val Thr	
		320 325 330 335	
10		atc ctc aac gtg ctg atg aac ccc acc cgc acc ggc ctc atc ctg acg	1056
		Ile Leu Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu Thr	
		340 345 350	
		ctg cag gaa atg ggc gcc gac atc gaa gtc atc aac ccg cgc ctt gcc	1104
		Leu Gln Glu Met Gly Ala Asp Ile Glu Val Ile Asn Pro Arg Leu Ala	
15		355 360 365	
		ggc ggc gaa gac gtg gcg gac ctg cgc gtt cgc tcc tcc acg ctg aag	1152
		Gly Gly Glu Asp Val Ala Asp Leu Arg Val Arg Ser Ser Thr Leu Lys	
		370 375 380	
		ggc gtc acg gtg ccg gaa gac cgc gcg cct tcg atg atc gac gaa tat	1200
20		Gly Val Thr Val Pro Glu Asp Arg Ala Pro Ser Met Ile Asp Glu Tyr	
		385 390 395	
		ccg att ctc gct gtc gcc gcc gcc ttc gcg gaa ggg gcg acc gtg atg	1248
		Pro Ile Leu Ala Val Ala Ala Ala Phe Ala Glu Gly Ala Thr Val Met	
		400 405 410 415	

002201-6126960

Asn Gly Leu Glu Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ser Ala

430

Val Ala Asn Gly Leu Lys Leu Asn Gly Val Asp Cys Asp Glu Gly Glu

445

Thr Ser Leu Val Val Arg Gly Arg Pro Asp Gly Lys Gly Leu Gly Asn

460

Ala Ser Gly Ala Ala Val Ala Thr His Leu Asp His Arg Ile Ala Met

475

Ser Phe Leu Val Met Gly Leu Val Ser Glu Asn Pro Val Thr Val Asp

gat gcc acg atg atc gcc acg agc ttc ccg gag ttc atg gac ctg atg 1536

Asp Ala Thr Met Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Leu Met

510

20 Ala Gly Leu Gly Ala Lys Ile Glu Leu Ser Asp Thr Lys Ala Ala

525

1587

25 <211> 33

<212> DNA

<213> Artificial Sequence

<220>

5 <223> Designed oligonucleotide primer to amplify DNA fragment having
partial sequence of soybean PPO gene

<400> 75

cacaggaaag gtacatggt ctgcatgcc cag 33

10

<210> 76

<211> 33

<212> DNA

<213> Artificial Sequence

15

<220>

<223> Designed oligonucleotide primer to amplify DNA fragment having
partial sequence of soybean PPO gene

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